CLAIMS

1. A full-length interferon gamma (IFNG) polypeptide variant exhibiting IFNG activity, wherein said variant comprises

(a) at least one amino acid substitution in a position selected from the group consisting of S132 and S142; and

(b) at least one amino acid substitution in a position selected from the group consisting of R137, R139 and R140.

2. The full-length variant according to claim 1, wherein said amino acid substitution is selected from the group consisting of S132P, S142P and S132P+S142P.

3. The full-length variant according to claim 2, wherein said amino acid substitution is S132P.

4. The full-length variant according to claim 2, wherein said amino acid substitution is S142P.

5. The full-length variant according to any of claims 1-4, wherein at least one non-positively charged amino acid residue is introduced by substitution in a position selected from the group consisting of R137, R139 and R140.

6. The full-length variant according to claim 5, wherein said non-positively charged amino acid residue is a proline residue.

7. The full-length variant according to any of claims 1-2 or 4-6, wherein said variant comprises the following substitutions: R137P+R139P+S142P.

8. The full-length variant according to any of claims 1-2 or 4-6, wherein said variant comprises the following substitutions: R137P+S142P

9. The full-length variant according to any of claims 1-3 or 5-6, wherein said variant comprises the following substitutions: S132P+R137P+R140P.

10. The full-length variant according to any of claims 1-3 or 5-6, wherein said variant comprises the following substitutions: S132P+R140P.

11. A full-length interferon gamma (IFNG) polypeptide variant exhibiting IFNG activity, wherein said variant comprises an amino acid substitution in position R137 and an amino acid substitution in position R140.

12. The full-length variant according to claim 11, wherein said variant comprises the substitutions R137X + R140P, wherein X is any amino acid residue, except arginine and lysine.

13. The full-length variant according to claim 11, wherein said variant comprises the substitutions R137P + R140X, wherein X is any amino acid residue, except arginine.

14. The full-length variant according to any of claims 11-13, wherein said variant comprises the substitutions R137P + R140P.

15. The full-length variant according to any of the preceding claims, wherein said variant comprises at least one further modification in the C-terminal part from amino acid residue S132 to amino acid residue Q143.

16. The full-length variant according to claim 15, wherein said further modification comprises introduction of at least one cysteine residue.

17. The full-length variant according to claim 16, wherein said cysteine residue is covalently attached to a polymer molecule.

18. The full-length variant according to claim 17, wherein said polymer molecule is a linear or branched polyethylene glycol.

19. The full-length variant according to any of the preceding claims, wherein said variant comprises an amino acid sequence from residue no. 1 to residue no. 131, which comprises 1-10 modifications compared to amino acid residue no. 1 to residue no. 131 of huIFNG.

20. The full-length variant according to claim 19, wherein said modification is a substitution.

21. The full-length variant according to claim 19 or 20, wherein said variant comprises the substitution S99T.

22. The full-length variant according to any of the preceding claims, wherein said variant, in the amino acid sequence from residue no. 1 to residue no. 131, comprises at least one introduced and/or at least one removed amino acid residue comprising an attachment group for a non-polypeptide moiety.

23. The full-length variant according to claim 22, wherein said variant comprises at least one introduced glycosylation site.

24. The full-length variant according to claim 23, wherein said glycosylation site is an N-glycosylation site.

25. The full-length variant according to claim 24, wherein said N-glycosylation site is introduced in a position comprising an amino acid residue having at least 25% of its side chain exposed to the surface (as defined in Example 1 herein).

26. The full-length variant according to claim 25, wherein said N-glycosylation site is introduced in a position comprising an amino acid residue having at least 50% of its side chain exposed to the surface (as defined in Example 1 herein).

27. The full-length variant according to any of claims 24-26, wherein said N-glycosylation site is introduced by substitution.

28. The full-length variant according to claim 27, wherein said substitution is selected from the group consisting of G18S, G18T, E38N, E38N+S40T, K61S, K61T, S65N+Q67S, S65N+Q67T, N85S, N85T, K94N, Q106S and Q106T.

29. The full-length variant according to claim 28, wherein said substitution is selected from the group consisting of G18T, E38N+S40T, K61T, S65N+Q67T, N85T, K94N and Q106T.

30. The full-length variant according to claim 29, wherein said substitution is selected from the group consisting of G18T, E38N+S40T, K61T, S65N+Q67T and N85T.

31. The full-length variant according to claim 30, wherein said substitution is E38N+S40T.

32. The full-length variant according to claim 22, wherein said variant comprises at least one introduced cysteine residue.

33. The full-length variant according to claim 32, wherein said cysteine residue is introduced in a position comprising an amino acid residue having at least 25% of its side chain exposed to the surface (as defined in Example 1 herein).

34. The full-length variant according to claim 33, wherein said cysteine residue is introduced in a position comprising an amino acid residue having at least 50% of its side chain exposed to the surface (as defined in Example 1 herein).

35. The full-length variant according to any of claims 32-34, wherein said cysteine residue is introduced by substitution.

36. The full-length variant according to claim 35, wherein said substitution is selected from the group consisting of N10C, N16C, E38C, N59C, N83C, K94C, N104C and A124C.

37. The full-length variant according to claim 36, wherein said substitution is selected from the group consisting of N16C, N59C and N16C+N59C.

38. The full-length variant according to any of claims 32-37, wherein said cysteine residue is covalently attached to a polymer molecule.

39. The full-length variant according to claim 38, wherein said polymer molecule is a linear or branched polyethylene glycol.

40. The full-length variant according to claim 22, wherein said variant comprises at least one introduced N-glycosylation site and at least one introduced cysteine residue.

41. The full-length varaint according to claim 40, wherein said N-glycosylation site is introduced in a position as defined in any of claims 25-31 and said cysteine residue is introduced in a position as defined in any of claims 33-37.

42. The full-length variant according to any of claims 1-18, wherein said variant comprises an amino acid sequence from residue no. 1 to residue no. 131, which is identical to residue no. 1 to residue no. 131 of huIFNG.

43. The full-length variant according to claim 42, wherein said variant is un-glycosylated

44. The full-length variant according to any of claims 1-42, wherein said variant is glycosylated.

44. The full-length variant according to any of claims 1-22 or 32-39, wherein said variant is un-glycosylated.

45. A nucleotide sequence encoding the full-length variant as defined in any of claims 1-44.

46. An expression vector comprising a nucleotide sequence as defined in claim 45.

47. A host cell comprising a nucleotide sequence as defined in claim 45 or an expression vector according to claim 46.

48. The host cell according to claim 47, wherein said cell is a glycosylating cell.

49. The host cell according to claim 48, wherein said cell is a CHO cell.

50. A composition comprising a substantially homogenous population of a full-length IFNG variant as defined in any of claims 1-44

51. A pharmaceutical composition comprising the full-length variant as defined in any of claims 1-44 and a pharmaceutically acceptable diluent, carrier or adjuvant.

52. A full-length variant as defined in any of claims 1-44, a composition as defined in claim 50, or a pharmaceutical composition as defined in claim 51, for use as a medicament.

53. Use of a full-length variant as defined in any of claims 1-44, a composition as defined in claim 50, or a pharmaceutical composition as defined in claim 51, for the manufacture of a medicament for the treatment of interstitial pulmonary diseases.

54. The use according to claim 53, wherein said interstitial pulmonary disease is idiopathic pulmonary fibrosis.

55. Use according to claim 53 or 54, wherein said variant or pharmaceutical composition is administered subcutaneously.

56. A method for treating or preventing interstitial pulmonary diseases, said method comprising administering to a mammal, in particular a human being, in need thereof an effective amount of a full-length variant as defined in any of claims 1-44, a composition as defined in claim 50, or a pharmaceutical composition as defined in claim 51.

57. The method according to claim 56, wherein said interstitial pulmonary disease is idiopathic pulmonary fibrosis.

58. The method according to claim 56 or 57, wherein said variant or pharmaceutical composition is administered subcutaneously.

59. A method for producing a full-length IFNG polypeptide, said method comprising

i) cultivating a host cell as defined in claims 47-49 under conditions suitable for production of the IFNG polypeptide, and

ii) recovering the IFNG polypeptide.